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> O <
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IntelliGenetics
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file AA436049vs09646624-2.res made by spaul on Fri 9 Apr 104 11:38:08-PDT.

Query sequence being compared: aa436049 (1-449)
Number of sequences searched: 2
Number of scores above cutoff: 2

Results of the initial comparison of aa436049 (1-449) with:
File : US09646624C.pep

SCORE
STDEV

```
      N
  N  50-
  U
  M
  B
  E
  R
  O
  F  10-
  S
  E   5-
  Q
  U
  E
  N
  C
  E
  S   0-

100-

      |---|---|---|---|---|---|---|---|---|---|
      0   6   11  17  23  28  34  40  45  51
                                      -8-6-
                                        -1
                                        |51|
                                         **
```

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. aa436049 (1-449)						
US-09-646-624C-2 Sequence 2, Application US/09646624C						
1. US-09-646-624C-2	Sequence 2, Application U	282	51	52	1.41	1
	**** 1 standard deviation above mean ****					
2. US-09-646-624C-4	Sequence 4, Application U	281	50	51	0.00	1
	**** 0 standard deviation from mean ****					

Initial Score   = 51   Optimized Score   = 52   Significance = 1.41
Residue Identity = 90% Matches   = 50   Mismatches   = 5
Gaps   = 0   Conservative Substitutions = 0
Translation Frame= 1

```
GWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTMVCASVQEGGKDSCQGDSGGGPLVCNQSLQGII
180       190       200       210       220       230       240

              10          20
              X           IRHDGGGDSGGPLVCNQSLQGII
                          ||||||||||||||||||||||

SWGQDPCAITRKPGVYTKVCKYVDWIQEIMKNNXXTGPTHHSPSPSISTWCLVPVHSVNKKPXAKTLYEHSLG
30        40        50    X   60        70        80        90
||||||||||||||||||||||
SWGQDPCAITRKPGVYTKVCKYVDWIQEIMKNN
250       260       270       280   X

100
LLDYPRCCHLI
```

PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Translation Frame	6		
Mismatch penalty	6	Joining penalty	20
Gap penalty	5.00	Window size	449
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	50	51	0.71

Times:

	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 563
Number of sequences searched: 2
Number of scores above cutoff: 2

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.